J. ZARA

1635

RAW SEQUENCE LISTING   DATE: 12/28/2000
PATENT APPLICATION: US/09/544,776   TIME: 08:21:55

    Input Set : A:\471.app
    Output Set: N:\CRF3\12282000\I544776.raw

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JAN 1 0 2001

TECH CENTER 1600/2900

```
 4 <110> APPLICANT: Wei, Dong
 5         Halenbeck, Robert
 6         Williams, Lewis T.
 8 <120> TITLE OF INVENTION: NOVEL PROTEIN ASSOCIATED WITH CELL
 9         STRESS RESPONSE
11 <130> FILE REFERENCE: 200130.471/1561.003
13 <140> CURRENT APPLICATION NUMBER: 09/544,776
14 <141> CURRENT FILING DATE: 2000-04-07
16 <160> NUMBER OF SEQ ID NOS: 11
18 <170> SOFTWARE: FastSEQ for Windows Version 4.0
20 <210> SEQ ID NO: 1
21 <211> LENGTH: 2240
22 <212> TYPE: DNA
23 <213> ORGANISM: Homo sapiens
25 <400> SEQUENCE: 1
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27 ccacaaccgc ccgcggctct gagacgcggc cccggcggcg gcggcagcag ctgcagcatc     120
28 atctccaccc tccagccatg gaagacctgg accagtctcc tctggtctcg tcctcggaca     180
29 gcccaccccg gccgcagccc gcgttcaagt accagttcgt gagggagccc gaggacgagg     240
30 aggaagaaga ggaggaggaa gaggaggacg aggacgaaga cctggaggag ctggaggtgc     300
31 tggagaggaa gcccgccgcc gggctgtccg cggcccagt gcccaccgcc cctgccgccg      360
32 gcgcgcccct gatggacttc ggaaatgact tcgtgccgcc ggcgcccgg ggaccctgc       420
33 cggccgctcc ccccgtcgcc ccggagcggc agccgtcttg ggacccgagc ccggtgtcgt     480
34 cgaccgtgcc cgcgccatcc ccgctgtctg ctgccgcagt ctcgccctcc aagctccctg     540
35 aggacgacga gcctccggcc cggcctcccc ctcctccccc ggccagcgtg agcccccagg     600
36 cagagcccgt gtggacccg ccagccccgg ctcccgccgc gccccctcc accccggccg      660
37 cgcccaagcg cagggctc tcgggctcag tggttgttga cctcctgtac tggagagaca       720
38 ttaagaagac tggagtggtg tttggtgcca gcctattcct gctgctttca ttgacagtat     780
39 tcagcattgt gagcgtaaca gcctacattg ccttggccct gctctctgtg accatcagct     840
40 ttaggatata caagggtgtg atccaagcta tccagaaatc agatgaaggc cacccattca     900
41 gggcatatct ggaatctgaa gttgctatat ctgaggagtt ggttcagaag tacagtaatt     960
42 ctgctcttgg tcatgtgaac tgcacgataa aggaactcag gcgcctcttc ttagttgatg    1020
43 attttagttga ttctctgaag tttgcagtgt tgatgtgggt atttacctat gttggtgcct    1080
44 tgtttaatgg tctgacacta ctgattttgg ctctcatttc actcttcagt gttcctgtta    1140
45 tttatgaacg gcatcaggca cagatagatc attatctagg acttgcaaat aagaatgtta    1200
46 aagatgctat ggctaaaatc caagcaaaaa tccctggatt gaagcgcaaa gctgaatgaa    1260
47 aacgcccaaa ataattagta ggagttcatc tttaaagggg atattcattt gattatacgg    1320
48 gggagggtca gggaagaacg aaccttgacg ttgcagtgca gtttcacaga tcgttgttag    1380
49 atctttattt ttagccatgc actgttgtga ggaaaaatta cctgtcttga ctgccatgtg    1440
50 ttcatcatct taagtattgt aagctgctat gtatggattt aaaccgtaat catatctttt    1500
51 tcctatctga ggcactggtg gaataaaaaa cctgtatatt ttactttgtt gcagatagtc    1560
52 ttgccgcatc ttggcaagtt gcagagatgg tggagctaga aaaaaaaaaa aaaaagccct    1620
53 tttcagtttg tgcactgtgt atggtccgtg tagattgatg cagatttttct gaaatgaaat    1680
54 gtttgtttag acgagatcat accggtaaag caggaatgac aaagcttgct tttctggtat    1740
55 gttctaggtg tattgtgact tttactgtta tattaattgc caatataagt aaatatagat    1800
56 tatatatgta tagtgtttca caaagcttag acctttacct tccagccacc ccacagtgct    1860
57 tgatatttca gagtcagtca ttggttatac atgtgtagtt ccaaagcaca taagctagaa    1920
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58 guagaaatat ttctaggagc actaccatct gttttcaaca tgaaatgcca cacacataga     1980
59 actccaacaa catcaatttc attgcacaga ctgactgtag ttaattttgt cacagaatct     2040
60 atggactgaa tctaatgctt ccaaaaatgt tgtttgtttg caaatatcaa acattgttat     2100
61 gcaagaaatt attaattaca aaatgaagat ttataccatt gtggtttaag ctgtactuaa     2160
62 ctaaatctgt ggaatgcatt gtgaactgta aaagcaaagt atcaataaag cttatagact     2220
63 taaaaaaaaa aaaaaaaaaa                                                  2240
65 <210> SEQ ID NO: 2
66 <211> LENGTH: 373
67 <212> TYPE: PRT
68 <213> ORGANISM: Homo sapien
70 <400> SEQUENCE: 2
71 Met Glu Asp Leu Asp Gln Ser Pro Leu Val Ser Ser Ser Asp Ser Pro
72  1               5                   10                  15
73 Pro Arg Pro Gln Pro Ala Phe Lys Tyr Gln Phe Val Arg Glu Pro Glu
74              20                  25                  30
75 Asp Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Asp Glu Asp Glu Asp
76          35                  40                  45
77 Leu Glu Glu Leu Glu Val Leu Glu Arg Lys Pro Ala Ala Gly Leu Ser
78      50                  55                  60
79 Ala Ala Pro Val Pro Thr Ala Pro Ala Ala Gly Ala Pro Leu Met Asp
80 65                  70                  75                  80
81 Phe Gly Asn Asp Phe Val Pro Pro Ala Pro Arg Gly Phe Leu Pro Ala
82                  85                  90                  95
83 Ala Pro Pro Val Ala Pro Glu Arg Gln Pro Ser Trp Asp Pro Ser Pro
84              100                 105                 110
85 Val Ser Ser Thr Val Pro Ala Pro Ser Phe Leu Ser Ala Ala Ala Val
86          115                 120                 125
87 Ser Pro Ser Lys Leu Pro Glu Asp Asp Glu Pro Pro Ala Arg Pro Pro
88          130                 135                 140
89 Pro Pro Pro Pro Ala Ser Val Ser Pro Gln Ala Glu Pro Val Trp Thr
90 145                 150                 155                 160
91 Pro Pro Ala Pro Ala Pro Ala Ala Pro Pro Ser Thr Pro Ala Ala Pro
92                  165                 170                 175
93 Lys Arg Arg Gly Ser Ser Gly Ser Val Val Val Asp Leu Leu Tyr Trp
94              180                 185                 190
95 Arg Asp Ile Lys Lys Thr Gly Val Val Phe Gly Ala Ser Leu Phe Leu
96       195                 200                 205
97 Leu Leu Ser Leu Thr Val Phe Ser Ile Val Ser Val Thr Ala Tyr Ile
98      210                 215                 220
99 Ala Leu Ala Leu Leu Ser Val Thr Ile Ser Pro Arg Ile Tyr Lys Gly
100 225                 230                 235                 240
101 Val Ile Gln Ala Ile Gln Lys Ser Asp Glu Gly His Pro Phe Arg Ala
102                 245                 250                 255
103 Tyr Leu Glu Ser Glu Val Ala Ile Ser Glu Glu Leu Val Gln Lys Tyr
104              260                 265                 270
105 Ser Asn Ser Ala Leu Gly His Val Asn Cys Thr Ile Lys Glu Leu Arg
106          275                 280                 285
107 Arg Leu Phe Leu Val Asp Asp Leu Val Asp Ser Leu Lys Phe Ala Val
108      290                 295                 300
```

```
109 Leu Met Trp Val Phe Thr Tyr Val Gly Ala Leu Phe Asn Gly Leu Thr
110 305             310             315             320
111 Leu Leu Ile Leu Ala Leu Ile Ser Leu Phe Ser Val Pro Val Ile Tyr
112             325             330             335
113 Glu Arg His Gln Ala Gln Ile Asp His Tyr Leu Gly Leu Ala Asn Lys
114             340             345             350
115 Asn Val Lys Asp Ala Met Ala Lys Ile Gln Ala Lys Ile Pro Gly Leu
116             355             360             365
117 Lys Arg Lys Ala Glu
118     370
120 <210> SEQ ID NO: 3
121 <211> LENGTH: 25
122 <212> TYPE: RNA
123 <213> ORGANISM: Artificial Sequence
125 <220> FEATURE:
126 <223> OTHER INFORMATION: Antisense oligonucleotide
128 <400> SEQUENCE: 3
129 cuggauagcu uggaucacac ccuug                            25
131 <210> SEQ ID NO: 4
132 <211> LENGTH: 25
133 <212> TYPE: RNA
134 <213> ORGANISM: Artificial Sequence
136 <220> FEATURE:
137 <223> OTHER INFORMATION: Antisense oligonucleotide
139 <400> SEQUENCE: 4
140 caacuucagg auuccagaua ugccc                            25
142 <210> SEQ ID NO: 5
143 <211> LENGTH: 24
144 <212> TYPE: RNA
145 <213> ORGANISM: Artificial Sequence
147 <220> FEATURE:
148 <223> OTHER INFORMATION: Antisense oligonucleotide
150 <400> SEQUENCE: 5
151 auuccaccag ugccucagau agga                             24
153 <210> SEQ ID NO: 6
154 <211> LENGTH: 24
155 <212> TYPE: RNA
156 <213> ORGANISM: Artificial Sequence
158 <220> FEATURE:
159 <223> OTHER INFORMATION: Antisense oligonucleotide
161 <400> SEQUENCE: 6
162 augaucuauc ugugccugau gccg                             24
164 <210> SEQ ID NO: 7
165 <211> LENGTH: 356
166 <212> TYPE: PRT
167 <213> ORGANISM: Homo sapiens
169 <400> SEQUENCE: 7
170 Met Ala Ala Glu Asp Ala Leu Pro Ser Gly Tyr Val Ser Phe Gly His
171 1               5               10              15
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172 Val Gly Gly Pro Pro Pro Ser Pro Ala Ser Pro Ser Ile Gln Tyr Ser
173              20              25              30
174 Ile Leu Arg Glu Glu Arg Glu Ala Glu Leu Asp Ser Glu Leu Ile Ile
175          35          40          45
176 Glu Ser Cys Asp Ala Ser Ser Ala Ser Glu Glu Ser Pro Lys Arg Glu
177      50          55          60
178 Gln Asp Ser Pro Pro Met Lys Pro Ser Ala Leu Asp Ala Ile Arg Glu
179 65              70              75              80
180 Glu Thr Gly Val Arg Ala Glu Glu Arg Ala Pro Ser Arg Arg Gly Leu
181              85              90              95
182 Ala Glu Pro Gly Ser Phe Leu Asp Tyr Pro Ser Thr Glu Pro Gln Pro
183          100             105             110
184 Gly Pro Glu Leu Pro Pro Gly Asp Gly Ala Leu Glu Pro Glu Thr Pro
185          115             120             125
186 Met Leu Pro Arg Lys Pro Glu Glu Asp Ser Ser Ser Asn Gln Ser Pro
187      130             135             140
188 Ala Ala Thr Lys Gly Pro Gly Pro Leu Gly Pro Gly Ala Pro Pro Pro
189 145             150             155             160
190 Leu Leu Phe Leu Asn Lys Gln Lys Ala Ile Asp Leu Leu Tyr Trp Arg
191              165             170             175
192 Asp Ile Lys Gln Thr Gly Ile Val Phe Gly Ser Phe Leu Leu Leu Leu
193          180             185             190
194 Phe Ser Leu Thr Gln Phe Ser Val Val Ser Val Val Ala Tyr Leu Ala
195          195             200             205
196 Leu Ala Ala Leu Ser Ala Thr Ile Ser Phe Arg Ile Tyr Lys Ser Val
197      210             215             220
198 Leu Gln Ala Val Gln Lys Thr Asp Glu Gly His Pro Phe Lys Ala Tyr
199 225             230             235             240
200 Leu Glu Leu Glu Ile Thr Leu Ser Gln Glu Gln Ile Gln Lys Tyr Thr
201          245             250             255
202 Asp Cys Leu Gln Phe Tyr Val Asn Ser Thr Leu Lys Glu Leu Arg Arg
203          260             265             270
204 Leu Phe Leu Val Gln Asp Leu Val Asp Ser Leu Lys Phe Ala Val Leu
205      275             280             285
206 Met Trp Leu Leu Thr Tyr Val Gly Ala Leu Phe Asn Gly Leu Thr Leu
207      290             295             300
208 Leu Leu Met Ala Val Val Ser Met Phe Thr Leu Pro Val Val Tyr Val
209 305             310             315             320
210 Lys His Gln Ala Gln Ile Asp Gln Tyr Leu Gly Leu Val Arg Thr His
211          325             330             335
212 Ile Asn Ala Val Val Ala Lys Ile Gln Ala Lys Ile Pro Gly Ala Lys
213      340             345             350
214 Arg His Ala Glu
215      355
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217 <210> SEQ ID NO: 8
218 <211> LENGTH: 371
219 <212> TYPE: PRT
220 <213> ORGANISM: Homo sapiens
222 <400> SEQUENCE: 8

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223 Met Glu Asp Leu Asp Gln Ser Pro Leu Val Ser Ser Ser Asp Ser Pro
224 1                   5                  10                  15
225 Pro Arg Pro Gln Pro Ala Phe Lys Tyr Gln Phe Val Arg Glu Pro Glu
226             20                  25                  30
227 Asp Glu Glu Glu Glu Glu Glu Glu Glu Glu Asp Glu Asp Glu Asp
228         35                  40                  45
229 Leu Glu Glu Leu Glu Val Leu Glu Arg Lys Pro Ala Ala Gly Leu Ser
230     50                  55                  60
231 Ala Ala Pro Val Pro Thr Ala Pro Ala Ala Gly Ala Pro Leu Met Asp
232 65                  70                  75                  80
233 Phe Gly Asn Asp Phe Val Pro Pro Ala Pro Arg Gly Pro Leu Pro Ala
234                 85                  90                  95
235 Ala Pro Pro Val Ala Pro Glu Arg Gln Pro Ser Trp Asp Pro Ser Pro
236             100                 105                 110
237 Val Ser Ser Thr Val Pro Ala Pro Ser Pro Leu Ser Ala Ala Ala Val
238         115                 120                 125
239 Ser Pro Ser Lys Leu Pro Glu Asp Asp Glu Pro Pro Ala Arg Pro Pro
240     130                 135                 140
241 Pro Pro Pro Pro Ala Ser Val Ser Pro Gln Ala Glu Pro Val Trp Thr
242 145                 150                 155                 160
243 Pro Pro Ala Pro Ala Pro Ala Ala Pro Pro Ser Thr Pro Ala Ala Pro
244                 165                 170                 175
245 Lys Arg Arg Gly Ser Ser Gly Ser Val Val Val Asp Leu Leu Tyr Trp
246             180                 185                 190
247 Arg Asp Ile Lys Lys Thr Gly Val Val Phe Gly Ala Ser Leu Phe Leu
248         195                 200                 205
249 Leu Leu Ser Leu Thr Val Phe Ser Ile Val Ser Val Thr Ala Tyr Ile
250     210                 215                 220
251 Ala Leu Ala Leu Leu Ser Val Thr Ile Ser Phe Arg Ile Tyr Lys Gly
252 225                 230                 235                 240
253 Val Ile Gln Ala Ile Gln Lys Ser Asp Glu Gly His Pro Phe Arg Ala
254                 245                 250                 255
255 Tyr Leu Glu Ser Glu Val Ala Ile Ser Glu Glu Leu Val Gln Lys Tyr
256             260                 265                 270
257 Ser Asn Ser Ala Leu Gly His Val Asn Cys Thr Ile Lys Glu Leu Arg
258         275                 280                 285
259 Arg Leu Phe Leu Val Asp Asp Leu Val Asp Ser Leu Lys Phe Ala Val
260     290                 295                 300
261 Leu Met Trp Val Phe Thr Tyr Val Gly Ala Leu Phe Asn Gly Leu Thr
262 305                 310                 315                 320
263 Leu Leu Ile Leu Ala Leu Ile Ser Leu Phe Ser Val Pro Val Ile Tyr
264                 325                 330                 335
265 Glu Arg His Gln Ala Gln Ile Asp His Tyr Leu Gly Leu Ala Asn Lys
266             340                 345                 350
267 Asn Val Lys Asp Ala Met Ala Lys Ile Gln Ala Lys Ile Pro Gly Leu
268         355                 360                 365
269 Lys Arg Lys
270     370
272 <210> SEQ ID NO: 9
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VERIFICATION SUMMARY   DATE: 12/28/2000
PATENT APPLICATION:- US/09/544,776   TIME: 08:21:56

Input Set : A:\471.app
Output Set: N:\CRF3\12282000\I544776.raw